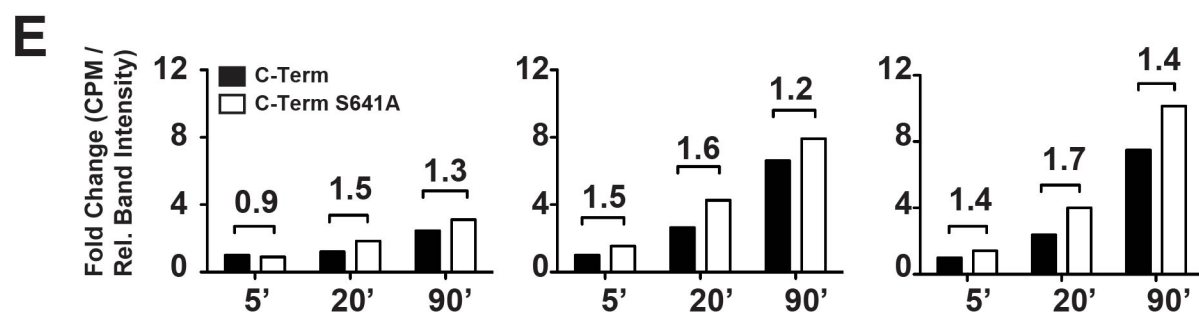
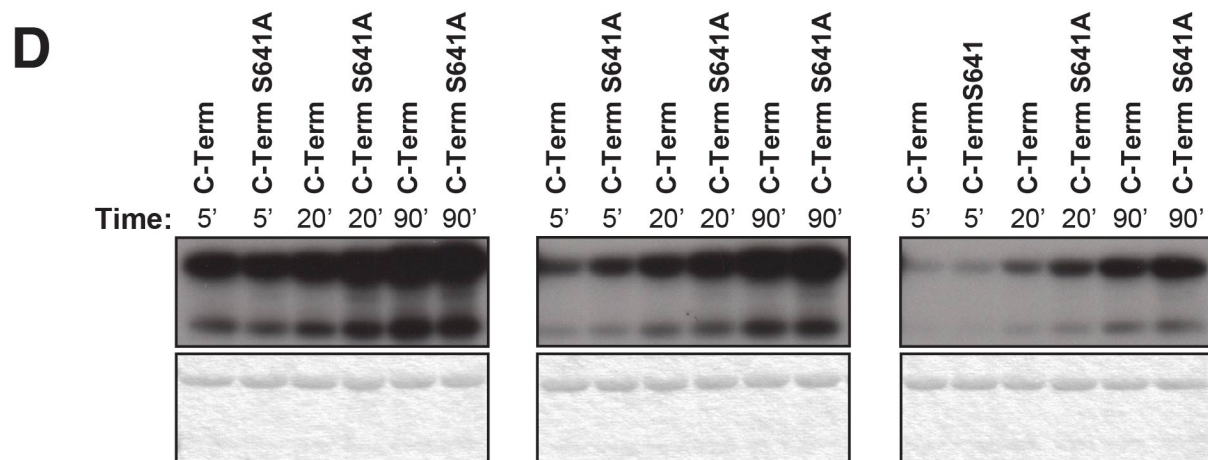
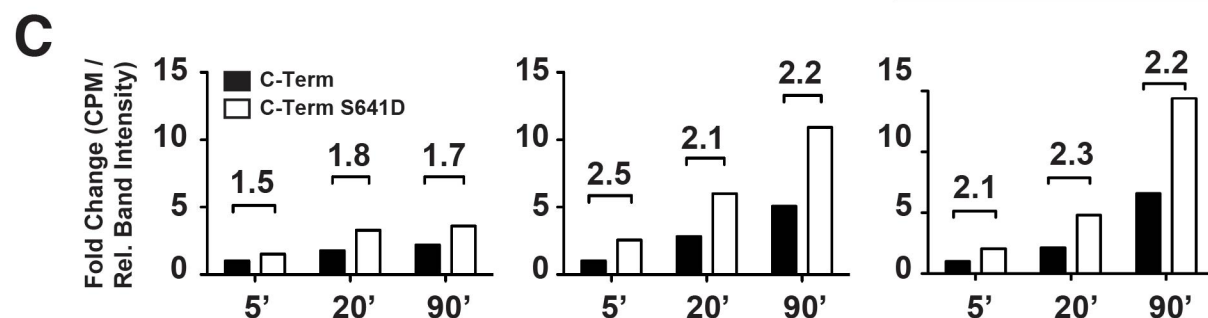
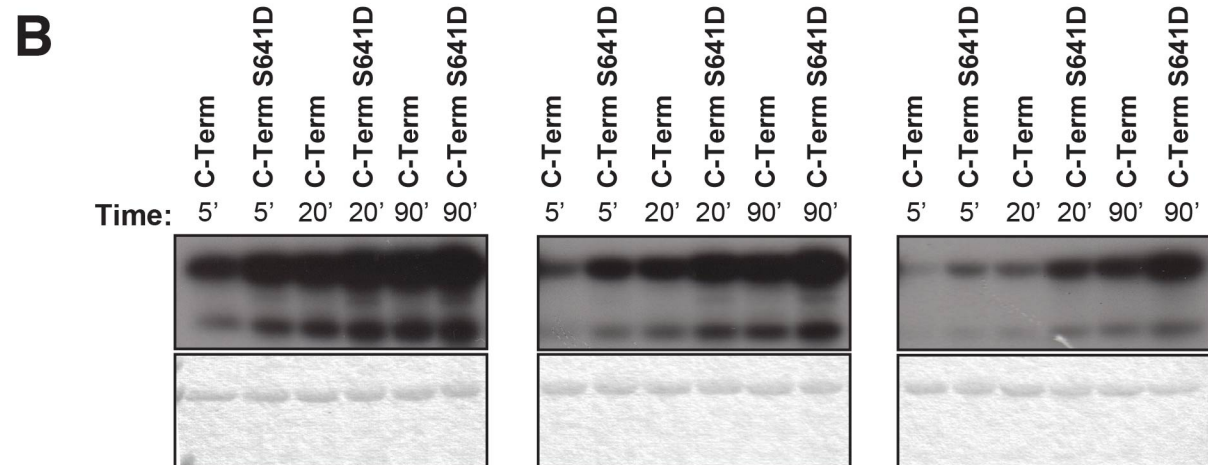
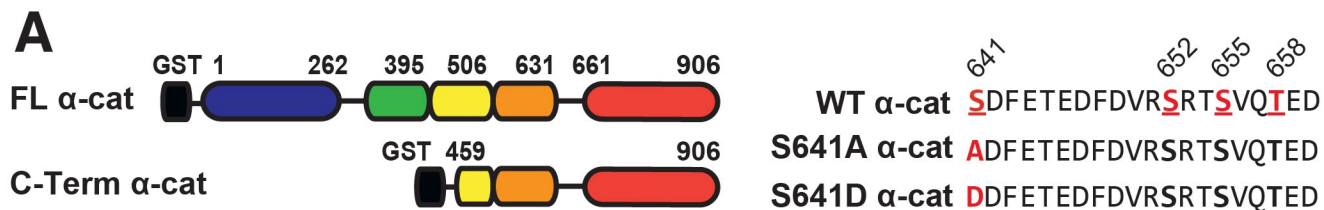


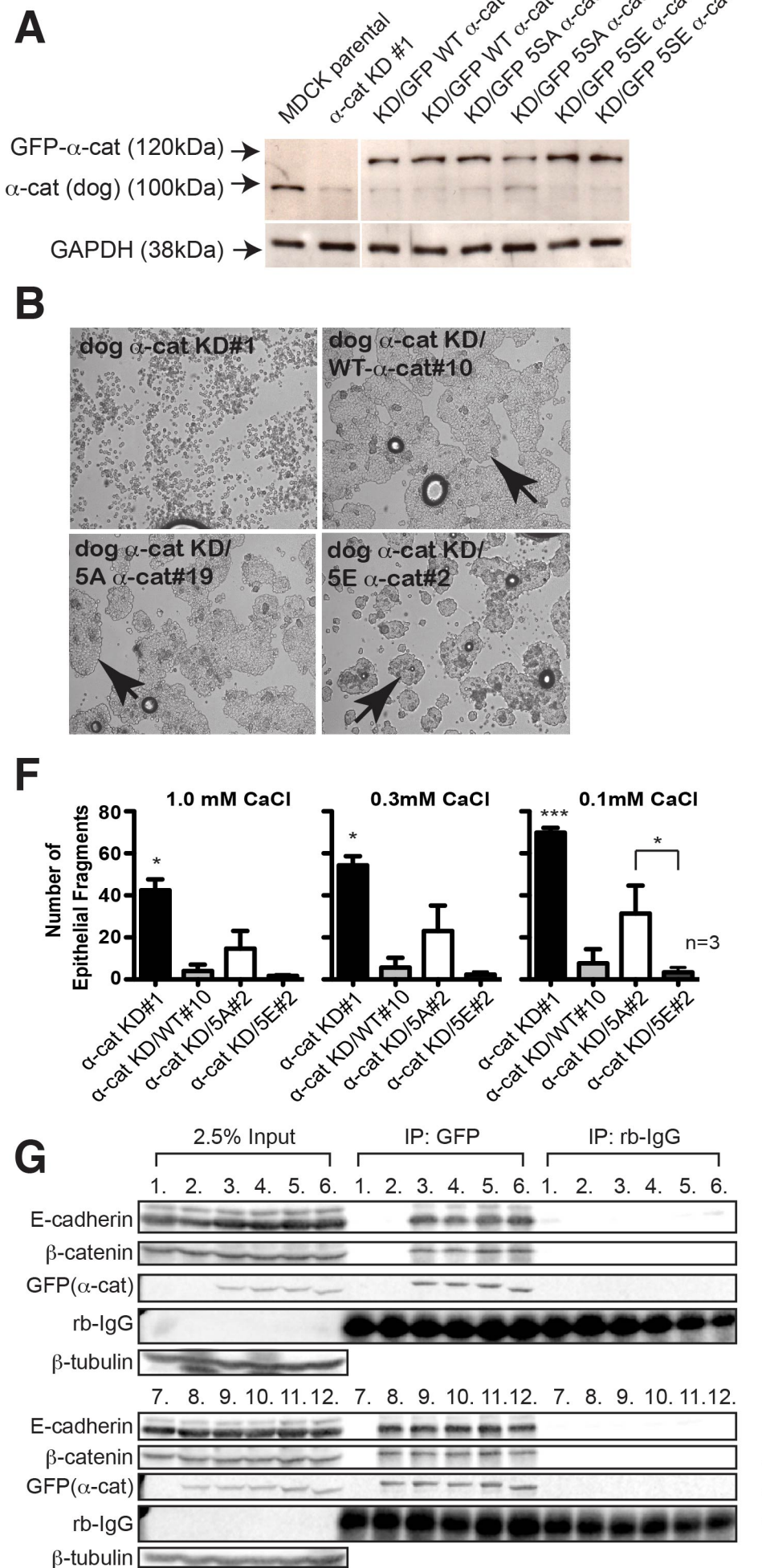
## Supplemental Figures for Escobar, Desai et al.,

### **Fig. S1: S641D fails to enhance phosphorylation by CK1 in a $\alpha$ E-cat C-terminal fragment.**

**A)** Schematic of full-length (FL) GST- $\alpha$ E-cat and a C-terminal truncation (C-term, amino acids 450-906) GST- $\alpha$ E-cat, as well as S641A and S641D phospho-mutant and -mimic mutations on  $\alpha$ E-cat. **B)** Autoradiograph of [ $\gamma$ - $^{32}$ P]-ATP in vitro kinase labeling of recombinant FL and S641D C-term  $\alpha$ E-cat. Time course is shown in minutes ('). Coomassie-stained gel bands of purified GST-tagged  $\alpha$ E-cat proteins shown below. **C)** Quantification of (B), as described in Fig. 2. Columns represent three independent experiments over more than one protein preparation. Numeric value of the relative fold-increase shown. **D)** Autoradiograph of [ $\gamma$ - $^{32}$ P]-ATP in vitro kinase labeling of recombinant FL and S641A C-term  $\alpha$ E-cat. **E)** Quantification of (D) as described in Fig. 2. Columns represent three independent experiments over more than one protein preparation. Numeric value of relative fold-increase shown.

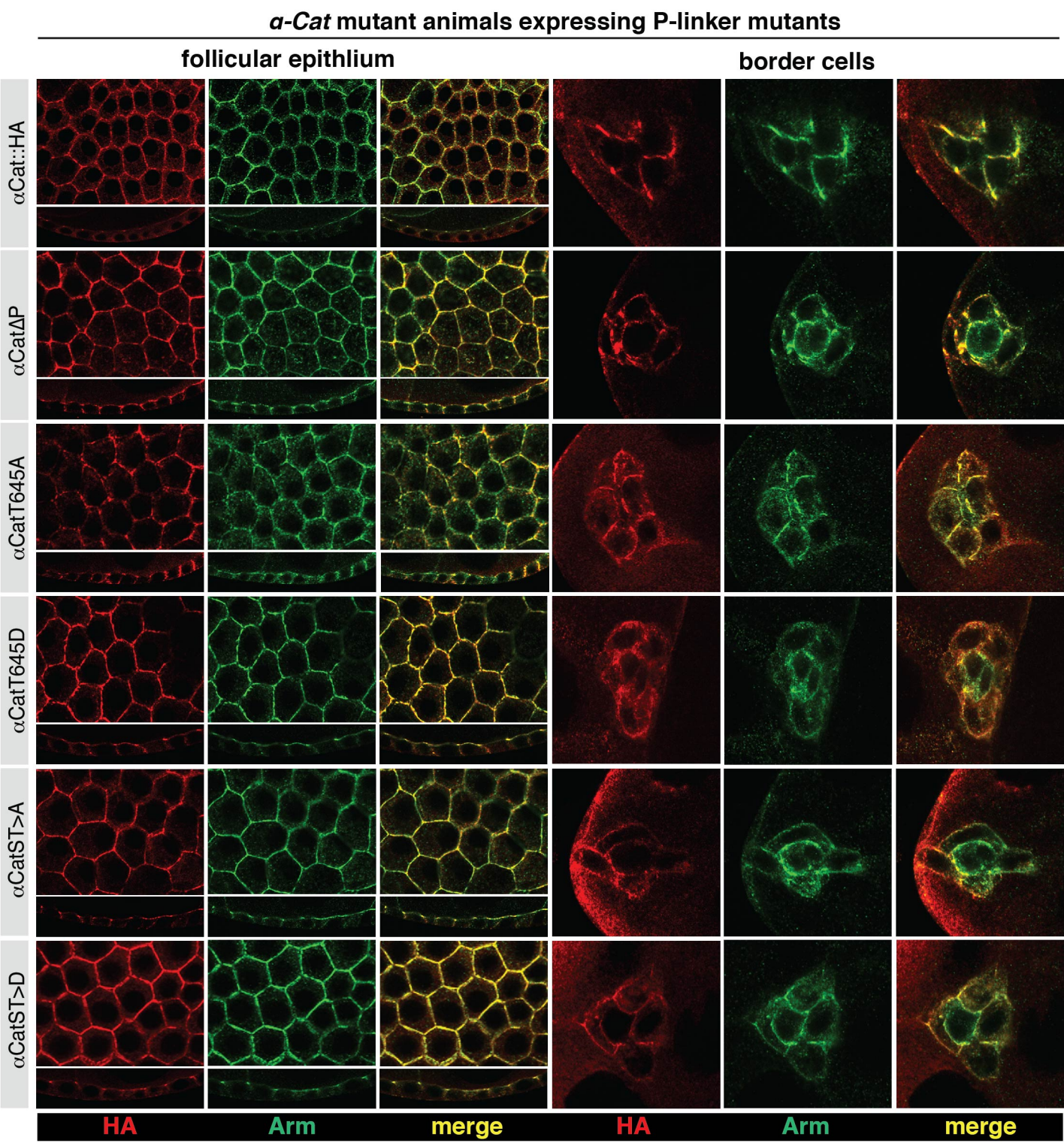


**Fig. S2: Phospho-domain charge status does not impact cell aggregation or cadherin/catenin complex assembly.** **A)** Western blot showing MDCK knock down (KD)/reconstitution cell clones. These are independent clonal lines of those shown in Fig. 3. **B)** Image of hanging drop aggregation assay. Aggregates are quantified by the number of particles greater than threshold (5 cells per aggregation particle (**C**)) and distribution of aggregate particles arranged by percent of particles displaying <4, 5-100 or >100 cells per particle (**D**). Error bars represent standard error of the mean of three technical replicates. Similar results were observed for independent replicates. **F)** Neutral protease (Dispase) Mechanical Disruption Assay, in the presence of a range of low (0.1 mM) to normal (1.0 mM) calcium. Y-axis reflects the number of macroscopic epithelial fragments counted after shaking (Methods). Error bars represent standard error of the mean from three independent experiments performed on per cell line. **G)** Western blot of MDCK knock down (KD)/reconstitution cell clones immunoprecipitated with antibodies to GFP and probed for  $\beta$ -catenin and E-cadherin. Statistical significance was assessed by Student's t-test, where  $p < 0.05$  (\*) or  $p < 0.001$  (\*\*\*)).



**Fig. S3: Expression of *Drosophila*  $\alpha$ Cat P-linker mutants in the follicular epithelium and border cells.** Ovaries of adult survivors from whole animal rescue experiments (see Figure 5A) were stained for HA to detect transgenic constructs and Armadillo (Arm). Left panels show face on and side views of the follicular epithelium whereas right panels show border cell clusters during migration. Distribution of P-linker mutants isoform of  $\alpha$ Cat is similar to that of  $\alpha$ Cat::HA or Arm.

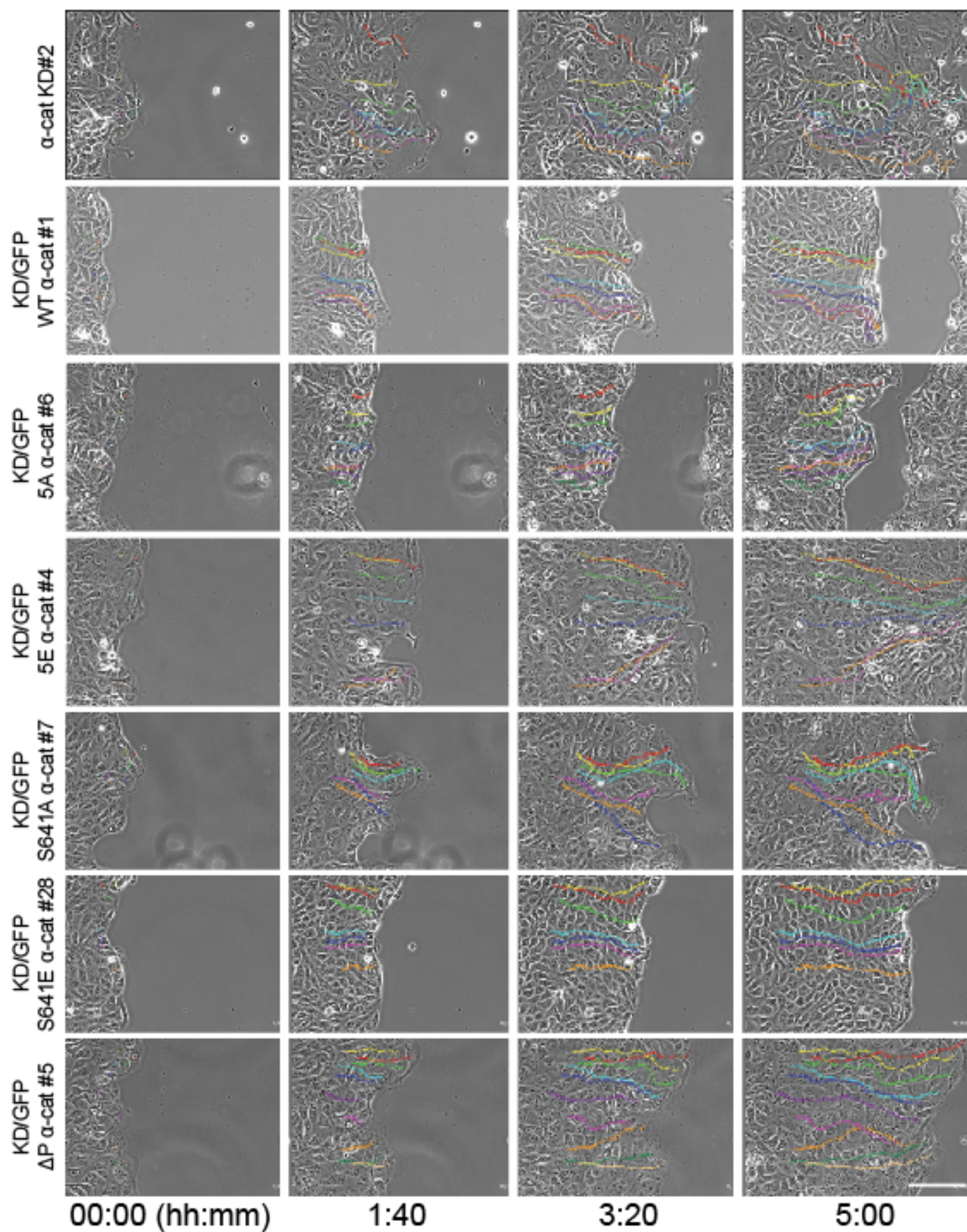




**Fig. S4: Representative movie time points from MDCK sheet migrations.**

Montage representing selected movie time-points (00:00, 01:40, 03:20, and 05:00 hours) during MDCK sheet migration analysis. One representative cell line for each GFP:: $\alpha$ E-cat construct is shown. Colored tracks represent paths of individual cells in the wound front. Scale bar, 100  $\mu$ m.







**Fig. S5: Mutation within the P-linker of  $\alpha$ E-cat does not affect steady-state localization of afadin or recognition by conformation-dependent  $\alpha$ E-cat antibody ( $\alpha$ 18), and trypsinolysis of purified  $\alpha$ E-cat proteins.** **A-C)** Localization of  $\alpha$ 18 conformation-dependent antibody in MDCK cells expressing wild-type (KD/WT#1), phospho-mutation (KD/5A#6) or phospho-mimic  $\alpha$ E-cat (KD/5E#4), shown in z-stack confocal sections. **D)** Quantification of (A-C) in terms of  $\alpha$ 18 intensity (arbitrary units, A.U.) per cell. **E-G)** Cellular localization of GFP- $\alpha$ E-cat and afadin (upper panels) and localization of Proximity Ligation Assay (PLA) signal between  $\alpha$ E-cat and afadin (lower panels) along sites of cell-cell contact is shown in z-stack confocal sections in MDCK cells expressing wildtype (KD/WT#1), phospho-mutant (KD/5A#6) or phospho-mimic (KD/5E#4)  $\alpha$ E-cat. **H)** Quantification of afadin intensity in (E-G), in terms of A.U. per cell. **I)** Quantification of PLA signal intensity in (E-G), in terms of A.U. per cell. No difference in PLA signal intensity due to phospho-mutation or phospho-mimic  $\alpha$ E-cat was observed. Fluorescence intensity quantifications based on at least 3 or more fields of view. **J)** Limited proteolysis of GST-affinity purified, thrombin-cleaved WT-, 5A- or 5D-  $\alpha$ E-cat proteins. Coomassie-stained SDS-PAGE of proteins incubated for time indicated with 0.01 mg/mL trypsin. This gel represents the experiment that was subjected to N-terminal sequencing, as in (Fig. 7E).

